

0590  
1212

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OIPE

## RAW SEQUENCE LISTING

DATE: 12/05/2001

PATENT APPLICATION: US/09/992,647

TIME: 10:27:53

Input Set : A:\pc0052cip\_seqlist.txt

Output Set: N:\CRF3\11212001\I992647.raw

**ENTERED**

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2 <110> APPLICANT: Xu, Hong
3      Cohan, Victoria L.
4      Stuart, Susan G.
6 <120> TITLE OF INVENTION: HUMAN EMR1-LIKE G PROTEIN-COUPLED RECEPTOR
8 <130> FILE REFERENCE: PC-0052 CIP
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/992,647
C--> 11 <141> CURRENT FILING DATE: 2002-11-13
13 <160> NUMBER OF SEQ ID NOS: 12
14 <170> SOFTWARE: PERL Program
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17 <211> LENGTH: 652
18 <212> TYPE: PRT
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: misc_feature
23 <223> OTHER INFORMATION: Incyte ID No: 429905
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28 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
29      20          25          30
30 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
31      35          40          45
32 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
33      50          55          60
34 Pro Leu Glu Thr Cys Asn Asp Ile Asn Glu Cys Thr Pro Pro Tyr
35      65          70          75
36 Ser Val Tyr Cys Gly Phe Asn Ala Val Cys Tyr Asn Val Glu Gly
37      80          85          90
38 Ser Phe Tyr Cys Gln Cys Val Pro Gly Tyr Arg Leu His Ser Gly
39      95          100         105
40 Asn Glu Gln Phe Ser Asn Ser Asn Glu Asn Thr Cys Gln Asp Thr
41      110         115         120
42 Thr Ser Ser Lys Thr Thr Gln Gly Arg Lys Glu Leu Gln Lys Ile
43      125         130         135
44 Val Asp Lys Phe Glu Ser Leu Leu Thr Asn Gln Thr Leu Trp Arg
45      140         145         150
46 Thr Glu Gly Arg Gln Glu Ile Ser Ser Thr Ala Thr Thr Ile Leu
47      155         160         165
48 Arg Asp Val Glu Ser Lys Val Leu Glu Thr Ala Leu Lys Asp Pro
49      170         175         180
50 Glu Gln Lys Val Leu Lys Ile Gln Asn Asp Ser Val Ala Ile Glu
51      185         190         195
52 Thr Gln Ala Ile Thr Asp Asn Cys Ser Glu Glu Arg Lys Thr Phe
53      200         205         210
54 Asn Leu Asn Val Gln Met Asn Ser Met Asp Ile Arg Cys Ser Asp
55      215         220         225

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56 Ile Ile Gln Gly Asp Thr Gln Gly Pro Ser Val Ile Ala Phe Ile
57                               230                235                240
58 Ser Tyr Ser Ser Leu Gly Asn Ile Ile Asn Ala Thr Phe Phe Glu
59                               245                250                255
60 Glu Met Asp Lys Lys Asp Gln Val Tyr Leu Asn Ser Gln Val Val
61                               260                265                270
62 Ser Ala Ala Ile Gly Pro Lys Arg Asn Val Ser Leu Ser Lys Ser
63                               275                280                285
64 Val Thr Leu Thr Phe Gln His Val Lys Met Thr Pro Ser Thr Lys
65                               290                295                300
66 Lys Val Phe Cys Val Tyr Trp Lys Ser Thr Gly Gln Gly Ser Gln
67                               305                310                315
68 Trp Ser Arg Asp Gly Cys Phe Leu Ile His Val Asn Lys Ser His
69                               320                325                330
70 Thr Met Cys Asn Cys Ser His Leu Ser Ser Phe Ala Val Leu Met
71                               335                340                345
72 Ala Leu Thr Ser Gln Glu Glu Asp Pro Val Leu Thr Val Ile Thr
73                               350                355                360
74 Tyr Val Gly Leu Ser Val Ser Leu Leu Cys Leu Leu Leu Ala Ala
75                               365                370                375
76 Leu Thr Phe Leu Leu Cys Lys Ala Ile Gln Asn Thr Ser Thr Ser
77                               380                385                390
78 Leu His Leu Gln Leu Ser Leu Cys Leu Phe Leu Ala His Leu Leu
79                               395                400                405
80 Phe Leu Val Gly Ile Asp Arg Thr Glu Pro Lys Val Leu Cys Ser
81                               410                415                420
82 Ile Ile Ala Gly Ala Leu His Tyr Leu Tyr Leu Ala Ala Phe Thr
83                               425                430                435
84 Trp Met Leu Leu Glu Gly Val His Leu Phe Leu Thr Ala Arg Asn
85                               440                445                450
86 Leu Thr Val Val Asn Tyr Ser Ser Ile Asn Arg Leu Met Lys Trp
87                               455                460                465
88 Ile Met Phe Pro Val Gly Tyr Gly Val Pro Ala Val Thr Val Ala
89                               470                475                480
90 Ile Ser Ala Ala Ser Trp Pro His Leu Tyr Gly Thr Ala Asp Arg
91                               485                490                495
92 Cys Trp Leu His Leu Asp Gln Gly Phe Met Trp Ser Phe Leu Gly
93                               500                505                510
94 Pro Val Cys Ala Ile Phe Ser Ala Asn Leu Val Leu Phe Ile Leu
95                               515                520                525
96 Val Phe Trp Ile Leu Lys Arg Lys Leu Ser Ser Leu Asn Ser Glu
97                               530                535                540
98 Val Ser Thr Ile Gln Asn Thr Arg Met Leu Ala Phe Lys Ala Thr
99                               545                550                555
100 Ala Gln Leu Phe Ile Leu Gly Cys Thr Trp Cys Leu Gly Leu Leu
101                               560                565                570
102 Gln Val Gly Pro Ala Ala Gln Val Met Ala Tyr Leu Phe Thr Ile
103                               575                580                585
104 Ile Asn Ser Leu Gln Gly Phe Phe Ile Phe Leu Val Tyr Cys Leu

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105          590          595          600
106 Leu Ser Gln Gln Val Gln Lys Gln Tyr Gln Lys Trp Phe Arg Glu
107          605          610          615
108 Ile Val Lys Ser Lys Ser Glu Ser Glu Thr Tyr Thr Leu Ser Ser
109          620          625          630
110 Lys Met Gly Pro Asp Ser Lys Pro Ser Glu Gly Asp Val Phe Pro
111          635          640          645
112 Gly Gln Val Lys Arg Lys Tyr
113          650
115 <210> SEQ ID NO: 2
116 <211> LENGTH: 3350
117 <212> TYPE: DNA
118 <213> ORGANISM: Homo sapiens
120 <220> FEATURE:
121 <221> NAME/KEY: misc_feature
122 <223> OTHER INFORMATION: Incyte ID No: 429905
124 <220> FEATURE:
125 <221> NAME/KEY: unsure
126 <222> LOCATION: 3293
127 <223> OTHER INFORMATION: a, t, c, g, or other
129 <400> SEQUENCE: 2
130 gcgtgggata cccgtaccac agaaatgcag ggaccattgc ttcttccagg cctctgcttt 60
131 ctgctgagcc tctttggagc tgtgactcag aaaacccaaa ctctctgtgc taagtgcgcc 120
132 ccaaatgctt cctgtgtcaa taacactcac tgcacctgca accatggata tacttctgga 180
133 tctgggcaga aactattcac attccccctt gagacatgta acgacattaa tgaatgtaca 240
134 ccacctata gtgtatattg tggatttaac gctgtatgtt acaatgtcga aggaagtctc 300
135 tactgtcaat gtgtcccagg atatagactg cattctggga atgaacaatt cagtaattcc 360
136 aatgagaaca cctgtcagga caccacctcc tcaaagacaa cccagggcag gaaagagctg 420
137 caaaagattg tggacaaatt tgagtcaact ctaccaatc agactttatg gagaacagaa 480
138 gggagacaag aaatctcatc cacagctacc actattctcc gggatgtgga atcgaaagtt 540
139 ctagaaactg ccttgaaaga tccagaacaa aaagtctcga aaatccaaaa cgatagtgtg 600
140 gctattgaaa ctcaagcgat tacagacaat tgctctgaag aaagaaagac attcaacttg 660
141 aacgtccaaa tgaactcaat ggacatccgt tgcagtgaca tcatccaggg agacacacaa 720
142 ggtcccagtg tcattgcctt tatctcatat tcttctcttg gaaacatcat aaatgcaact 780
143 ttttttgaag agatggataa gaaagatcaa gtgtatctga actctcaggt tgtgagtgtc 840
144 gctattggac ccaaaaggaa cgtgtctctc tccaagtctg tgacgctgac tttccagcac 900
145 gtgaagatga ccccagtag caaaaaggtc ttctgtgtct actggaagag cacagggcag 960
146 ggcagccagt ggtccaggga tggctgcttc ctgatacacg tgaacaagag tcacaccatg 1020
147 tgtaattgca gtcacctgtc cagcttcgct gtccctgatg ccctgaccag ccaggaggag 1080
148 gatcccgtgc tgactgtcat cacctacgtg gggctgagcg tctctctgct gtgcctcctc 1140
149 ctggcgcccc tcacttttct cctgtgtaaa gccatccaga acaccagcac ctactgcat 1200
150 ctgcagctct cgctctgcct ctctctggcc caccctctct tctcgtggg gattgatcga 1260
151 actgaaccca aggtgctgtg ctccatcatc gccggtgctt tgcactatct ctacctggcc 1320
152 gccttcacct ggatgctgct ggagggtgtg caccctctcc tcactgcacg gaacctgaca 1380
153 gtggtcaact actcaagcat caatagactc atgaagtgga tcatgttccc agtcggctat 1440
154 ggcgttcccg ctgtgactgt ggcattttct gcagcctcct ggcctcacct ttatggaact 1500
155 gctgatcgat gctggctcca cctggaccag ggattcatgt ggagtttctc tggcccagtc 1560
156 tgtgccattt tctctgcgaa tttagtattg tttatcttgg tcttttggat tttgaaaaga 1620
157 aaactttcct ccctcaatag tgaagtgtca accatccaga acacaaggat gctggctttc 1680

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158 aaagcaacag ctcagctctt catcctgggc tgcacatggt gtctgggctt gctacaggtg 1740
159 ggtccagctg cccagggtcat ggcctacctc ttcacatca tcaacagcct ccaaggcttc 1800
160 ttcactcttct tgggtctactg cctcctcagc cagcaggtcc agaaacaata tcaaaagtgg 1860
161 tttagagaga tcgtaaaatc aaaatctgag tctgagacat acacactttc cagcaagatg 1920
162 ggtcctgact caaaacccag tgagggggat gtttttccag gacaagtga gaaaaatat 1980
163 taaaactaga atattcaact ccatatggaa aatcatatoc atggatctct ttggcattat 2040
164 gaagaatgaa gctaaggaaa aggggaattca ttaacatat catccttgga gaggaagtaa 2100
165 tcaaccttta cttcccaaac tgtttgttct ccacaatagg ctctcaacaa atgtgtggt 2160
166 aattgcattt ctcttcaacta tgggtgattc agtcaatgct tgtccctgga aacccaaagc 2220
167 atgaccactg caaatatttc cttgactttt tgtaaagaa gaggtccttt tcctcaagtt 2280
168 cttagtccca ctcactcctaa acttgctctt tttttaagac agagtttcac tctgtcacc 2340
169 aggtctggag gtatggcat gatcgtagct cactgcagcc tcaaaactca gagctcaact 2400
170 ggttctccag cctcagcttc ccaaagtgtc gggattacag gcatgagcca ctgcacctgg 2460
171 ccataaactt gctctttaaa ctcaactcatt cctcacaacc atcagcttcc tactggcttt 2520
172 acttccctgc tagatacagg ctaatttttt tttttttttt tttttttttt tgagatggag 2580
173 tttcgtctct gttgcccagg ctggagtgc aacggcgtgag tgcaacctct gcctcccggg 2640
174 ttcaagcgat tcttctgcct cagcctccca agtagctggc gttacaggta tggaccacca 2700
175 tgtccggcta attttgtatt tttagtagag acagggtttc tccatgttg tccaggtggt 2760
176 ctgcaactcc cagcctcagg tgatccacct gacttggcct cccaagagtg ctgggattac 2820
177 aggcattgag caccgtgccc agcccaggct aacttatttt cttctgagac tgagtctcac 2880
178 tactgtcacc caggctggag tgcagtgggt agatctaggg tcaactgcaac ctctacctcc 2940
179 tgggttcaag caattctcct gccttagcct ccgatagct gggactacaa gcacatgccg 3000
180 ccatgccag ctaattttgt attttttagt gagacaagg ttcacatgt tggccaggct 3060
181 gatctcaaac tcttgacctc aagcagcgat ccacctgcc gggcctccca aagtgtggtg 3120
182 attacagaca caagccatcg cgcctgatga gagattttta gtgttctcac cacaaaaaaa 3180
183 aagaaaaaaa agttatatga ggtaatcgta tattaattag cttgacttag tcattccacg 3240
W--> 184 atgtagatat atttcaaac atcctgttgt acatgataaa tatatatatt ttngtctata 3300
185 taaaacaaat aaataataaa atgtttaaag tgtaaaaaaa aaaaaaaaag 3350
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188 <211> LENGTH: 153
189 <212> TYPE: DNA
190 <213> ORGANISM: Homo sapiens
192 <220> FEATURE:
193 <221> NAME/KEY: misc_feature
194 <223> OTHER INFORMATION: Incyte ID No: 429905H1
196 <220> FEATURE:
197 <221> NAME/KEY: unsure
198 <222> LOCATION: 4, 8, 16, 19, 65
199 <223> OTHER INFORMATION: a, t, c, g, or other
201 <400> SEQUENCE: 3
W--> 202 ggtngctngc gtgggntanc cgtaccacag gaatccagg accattggtt ttttcagggc 60
W--> 203 tctgntttct gctgaggctc tttggagctg tgactcagaa aaccaaact tcctgtgcta 120
204 agtgcccccc aaatgcttcc tgtgtcaata aca 153
206 <210> SEQ ID NO: 4
207 <211> LENGTH: 320
208 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
211 <220> FEATURE:
212 <221> NAME/KEY: misc_feature

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Output Set: N:\CRF3\11212001\I992647.raw

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215 <400> SEQUENCE: 4
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217 gggaccattg cttcttccag gcctctgctt tctgctgagc ctctttggag ctgtgactca 120
218 gaaaaccaa acttctgtg ctaagtcccc cccaaatgct tcctgtgtca ataacactca 180
219 ctgcacctgc aaccatggat atacttctgg atctgggcag aaactattca cattccccctt 240
220 ggagacatgt aacgacatta atgaatgtac accaccctat agtgtatatt gtggatttaa 300
221 cgctgtgtgt tacaatgtcg                                     320
223 <210> SEQ ID NO: 5
224 <211> LENGTH: 624
225 <212> TYPE: DNA
226 <213> ORGANISM: Homo sapiens
228 <220> FEATURE:
229 <221> NAME/KEY: misc_feature
230 <223> OTHER INFORMATION: Incyte ID No: 8009216H1
232 <400> SEQUENCE: 5
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234 atacccttac cacagaaatg caggaccatt gcttcttcca ggcctctgct ttctgctgag 120
235 cctcttttga gctgtgactc agaaaaccaa aacttctgt gctaagtgcc ccccaaatgc 180
236 ttctgtgtgc aataacactc actgcacctg caaccatgga tatacttctg gatctgggca 240
237 gaaactattc acattccccct tggagacatg taacgacatt aatgaatgta caccacccta 300
238 tagtgtatat tgtggattta acgctgtgtg ttacaatgtc gaaggaagtt tctactgtca 360
239 atgtgtccca ggatatagac tgcattctgg gaatgaacaa ttcagtaatt ccaatgagaa 420
240 cacctgtcag gacaccacct cctcaaagac aaccagggc aggaaagagc tgcaaaagat 480
241 tgtggacaaa tttgagtcac ttctcaccaa tcagacttta tggagaacag aatggagaca 540
242 agaaatctca tccacaggta ccactattct ccgggatgtg gaatcgaaaag ttctagaaac 600
243 tggcttgaaa gatccagaac aaaa                                     624
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246 <211> LENGTH: 554
247 <212> TYPE: DNA
248 <213> ORGANISM: Homo sapiens
250 <220> FEATURE:
251 <221> NAME/KEY: misc_feature
252 <223> OTHER INFORMATION: Incyte ID No: 1837630T6
254 <400> SEQUENCE: 6
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256 ttcccttttc cttagcttca ttcttcataa tgccaaagag atccatggat atgattttcc 120
257 atatggagtt gaatattcta gttttaatat gttctcttca cttgtcctgg aaaaacatcc 180
258 ccctcactgg gttttgagtc aggaccatc ttgctggaaa gtgtgtatgt ctgactca 240
259 gattttgatt ttacgatctc gctaaaccac ttttgatatt gtttctggac ctgctggctg 300
260 aggaggcagt agaccaagaa gatgaagaag ccttgaggc tgttgatgat ggtgaagagg 360
261 taggcatga cctgggcagc tggaccacc tgtagcaagc ccagacacca tgtgcagccc 420
262 aggatgaaga gctgagctgt tgctttgaaa gccagcatcc ttgtgttctg gatggttgac 480
263 acttcactat tgagggagga aagttttctt ttcaaatcc aaaagaccaa gataaacaat 540
264 actaaattcg caga                                     554
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267 <211> LENGTH: 514
268 <212> TYPE: DNA
269 <213> ORGANISM: Homo sapiens

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## VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:202 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:357 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:11  
L:487 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:12